

### **Amendments to the Claims:**

The following list of claims will replace all prior versions of the claims in the application:

1. (*Currently amended*) A method of managing and retrieving biological data for efficient exploration and analysis, the method comprising:

acquiring and staging gene expression data for storage, wherein the gene expression data comprises hybridization experiment data from microarray samples prepared from tissues and cell lines;

providing storing the gene expression data in a data warehouse which comprises comprising three distinct databases comprising a gene expression database for storing quantitative gene expression measurements for the tissues and cell lines[[:]], a clinical database for storing sample data on bio-samples and donors ~~corresponding to~~ from which the tissues and cell lines were obtained[[:]], and a fragment index database for storing information on biological properties and gene sequences for DNA fragments ~~corresponding to the tissues and cell lines in~~ microarrays from which the gene expression measurements were obtained, wherein the data warehouse is arranged in a relational format, and wherein staging comprises linking gene expression measurements in the gene expression database with sample data in the clinical database and information in the fragment index database;

providing a user interface for entry of a first query, wherein the first query comprises a first sample set or gene set for which additional information is sought, and wherein the sample set comprises a plurality of samples having one or more selected attributes and the gene set comprises at least one gene having one or more selected properties;

receiving the first query;

correlating gene expression measurements within the gene expression database with the first sample set or gene set of the first query; and

displaying at the user interface the correlated gene expression measurements that are responsive to the first query.

2. (*Original*) The method of claim 1, wherein the data warehouse is constructed in a star relational schema.

3. (*Original*) The method of claim 1, wherein the data warehouse is constructed in a snowflake relational schema.

4. (*Currently amended*) The method of claim 1, ~~wherein the analysis comprises~~ further comprising a gene signature analysis ~~and the method further~~ that comprises analyzing the correlated gene expression measurements to identify a present set of DNA fragments that are ~~consistently expressed~~ present within the first sample set or gene set, and an absent set of DNA fragments that are ~~consistently not expressed~~ absent within the first sample set or gene set.

5. (*Currently amended*) The method of claim 4, ~~wherein the analysis comprises~~ further comprising a gene signature differential analysis ~~and the method further comprises that~~ comprises:

performing a gene signature analysis for a second sample set or gene set;

comparing the two different gene signature analysis results; and

identifying four sets of DNA gene fragments comprising:

a present/absent gene set including fragments that are ~~consistently expressed~~ present within the first sample set or gene set and ~~consistently not expressed~~ absent within the second sample set or gene set;

a present/present gene set including fragments that are ~~consistently expressed~~ present within both the first and second sample set or gene set;

an absent/absent gene set including fragments that are ~~consistently not expressed~~ absent within both the first and second sample set or gene set; and

an absent/present gene set including fragments that are ~~consistently not expressed~~ absent within the first sample set or gene set and are ~~consistently expressed~~ present within the second sample set or gene set.

6. (*Currently amended*) The method of claim 1, ~~wherein the analysis comprises~~ further comprising a fold change analysis ~~comprising~~ that comprises:

calculating mean expression levels for each gene fragment within the first sample set or gene set;

before or after calculating mean expression levels for the first sample set or gene set, correlating gene expression measurements with a second query comprising a second sample set or gene set;

calculating mean expression levels of each gene fragment within the second sample set or gene set; and

comparing the mean expression levels for the two sample sets or gene sets to quantify a change in expression for differentially expressed genes between pairs of DNA fragments.

7. *(Currently amended)* The method of claim 1, ~~wherein the analysis comprises~~ further comprising an E Northern analysis that identifies DNA fragments with regard to a pair of user-selected percentiles over the values for a sample.

8. *(Currently amended)* A computer system comprising:

a data warehouse ~~which~~ that comprises three distinct databases comprising a gene expression database for storing quantitative gene expression measurements obtained from microarray samples prepared from ~~for~~ tissues and cell lines~~[[;]]~~, a clinical database for storing sample data on bio-samples and donors ~~corresponding to~~ from which the tissues and cell lines were obtained~~[[;]]~~, and a fragment index database for storing information on biological properties and gene sequences for DNA fragments ~~corresponding to the tissues and cell lines on microarrays from which the gene expression measurements were obtained~~, wherein the data warehouse is arranged in a relational format;

a staging database for linking gene expression measurements in the gene expression database with sample data in the clinical database and information in the fragment index database;

a data explorer for accessing and analyzing data in the data warehouse; and

a user interface in communication with the data explorer for entering a first query, wherein the first query comprises a first sample set or gene set for which additional information is sought, and wherein the sample set comprises a plurality of samples having one or more

selected attributes and the gene set comprises at least one gene having one or more selected properties, and for displaying the results of a correlation of the gene expression measurements with the first sample set or gene set.

9. *(Original)* The computer of claim 8, wherein the data warehouse is constructed in a star relational schema.

10. *(Original)* The computer of claim 8, wherein the data warehouse is constructed in a snowflake relational schema.

11. *(Currently amended)* The computer of claim 8, wherein the data explorer performs a gene signature analysis comprising analyzing the correlated gene expression measurements to identify a present set of DNA fragments that are ~~consistently expressed~~ present within the first sample set or gene set, and an absent set of DNA fragments that are ~~consistently not expressed~~ absent within the first sample set or gene set.

12. *(Currently amended)* The computer of claim 11, wherein the data explorer performs a gene signature differential analysis comprising:

performing a gene signature analysis for a second sample set or gene set;

comparing the two different gene signature analysis results; and

identifying four sets of DNA gene fragments comprising:

a present/absent gene set including fragments that are ~~consistently expressed~~ present within the first sample set or gene set and ~~consistently not expressed~~ absent within the second sample set or gene set;

a present/present gene set including fragments that are ~~consistently expressed~~ present within both the first and second sample set or gene set;

an absent/absent gene set including fragments that are ~~consistently not expressed~~ absent within both the first and second sample set or gene set; and

an absent/present set including fragments that are ~~consistently not expressed~~  
absent within the first sample set or gene set and are ~~consistently expressed~~ present  
within the second sample set or gene set.

13. (*Previously presented*) The computer of claim 8, wherein the data explorer performs a fold change analysis, comprising:

calculating mean expression levels for each gene fragment within the first sample set or gene set;

before or after calculating mean expression levels for the first sample set or gene set, correlating gene expression measurements with a second query comprising a second sample set or gene set;

calculating mean expression levels of each gene fragment within the second sample set or gene set; and

comparing the mean expression levels for the two sample sets or gene sets to quantify a change in expression for differentially expressed genes between pairs of DNA fragments.

14. (*Previously presented*) The computer of claim 8, wherein the data explorer performs an E Northern analysis that identifies DNA fragments with regard to a pair of user-selected percentiles over the values for a sample.

15. (*Currently amended*) A computer program product comprising a computer-usable medium having computer-readable program code embodied thereon relating to a data warehouse comprising gene expression data and related information, the computer program product comprising computer-readable program code for effecting the following steps within a computing system:

arranging the data warehouse into three distinct databases comprising a gene expression database for storing quantitative gene expression measurements ~~for~~ taken from microarray samples prepared from tissues and cell lines, a clinical database for storing sample data on bio-samples and donors ~~corresponding to~~ from which the tissues and cell lines were obtained[[;]], and a fragment index database for storing information on biological properties and gene

sequences for DNA fragments corresponding to the tissues and cell lines on microarrays from which the gene expression measurements were obtained, wherein the data warehouse is arranged in a relational format;

providing a staging database for linking gene expression measurements in the gene expression database with sample data in the clinical database and information in the fragment index database;

providing a user interface for entry of a first query, wherein the first query comprises a first sample set or gene set for which additional information is sought, and wherein the sample set comprises a plurality of samples having one or more selected attributes and the gene set comprises at least one gene having one or more selected properties;

correlating gene expression measurements within the gene expression database with the sample set or gene set of the first query; and

displaying at the user interface the correlated gene expression measurements that are responsive to the first query.

16. *(Original)* The computer program product of claim 15, wherein the data warehouse is constructed in a star relational schema.

17. *(Original)* The computer program product of claim 15, wherein the data warehouse is constructed in a snowflake relational schema.

18. *(Currently amended)* The computer program product of claim 15, further comprising computer-readable program code for effecting a gene signature analysis comprising analyzing the correlated gene expression measurements to identify a present set of DNA fragments that are ~~consistently expressed~~ present within the first sample set or gene set, and an absent set of DNA fragments that are ~~consistently not expressed~~ absent within the first sample set or gene set.

19. *(Currently amended)* The computer program product of claim 18, further comprising computer-readable program code for effecting a gene signature differential analysis and the method further comprises:

performing a gene signature analysis for a second sample set or gene set;  
comparing the two different gene signature analysis results; and  
identifying four sets of DNA gene fragments comprising:

a present/absent gene set including fragments that are ~~consistently expressed~~  
present within the first sample set or gene set and ~~consistently not expressed~~ absent  
within the second sample set or gene set;

a present/present gene set including fragments that are ~~consistently expressed~~  
present within both the first and second sample set or gene set;

an absent/absent gene set including fragments that are ~~consistently not expressed~~  
absent within both the first and second sample set or gene set; and

an absent/present gene set including fragments that are ~~consistently not expressed~~  
absent within the first sample set or gene set and are ~~consistently expressed~~ present  
within the second sample set or gene set.

20. (*Previously presented*) The computer program product of claim 15, further  
comprising computer-readable program code for effecting a fold change analysis comprising:

calculating mean expression levels for each gene fragment within the first sample set or  
gene set;

before or after calculating mean expression levels for the first sample set or gene set,  
correlating gene expression measurements with a second query comprising a second sample set  
or gene set;

calculating mean expression levels of each gene fragment within the second sample set or  
gene set; and

comparing the mean expression levels for the two sample sets or gene sets to quantify a  
change in expression for differentially expressed genes between pairs of DNA fragments.

21. (*Previously presented*) The method of claim 15, further comprising computer-  
readable program code for effecting an E Northern analysis that identifies DNA fragments with  
regard to a pair of user-selected percentiles over the values for a sample.